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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Sep 06 16:59:15 EDT 2007

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Reviewer Comments:

<110> TŠRECI, ™zlem  
SAHIN, Ugar  
KREITER, Sebastian  
Johannes Gutenberg-Universit„t Mainz, vertreten durch den  
Pr„sidenten

Please remove all foreign accent marks: they are non-ASCII characters, and cannot be processed.

<210> 7  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Enzyme restriction site

Please try to clarify the above <223> response: can the source of the genetic material be mentioned? This type of response appears in Sequence 8.

<210> 11  
<211> 1962  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Nucleic acid encoding a fusion protein

The above <223> response needs clarification: what are the sources of the fusion protein? This type of response appears in Sequence 13, too.

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Application No: 10575640 Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-27 08:37:14.100  
Finished: 2007-08-27 08:37:17.698  
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 598 ms  
Total Warnings: 8  
Total Errors: 0  
No. of SeqIDs Defined: 66  
Actual SeqID Count: 66

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

<210> 1  
<211> 78  
<212> DNA  
<213> Homo sapiens

<400> 1  
atgcgggtca cggcgccccg aaccctcatc ctgctgctct cgggagccct ggcctgacc 60  
  
gagacctggg ccggctcc 78

<210> 2  
<211> 26  
<212> PRT  
<213> Homo sapiens

<400> 2  
  
Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala  
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser  
20 25

<210> 3  
<211> 168  
<212> DNA  
<213> Homo sapiens

<400> 3  
atcgtgggca ttgttgctgg cctggctgtc ctgacagttg tggtcacgg agctgtggtc 60  
  
gctactgtga tgtgtaggag gaagagctca ggtggaaaag gagggagcta ctctcaggct 120  
  
gcgtccagcg acagtgccca gggctctgat gtgtctctca cagcttga 168

<210> 4  
<211> 55  
<212> PRT  
<213> Homo sapiens

<400> 4  
  
Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile  
1 5 10 15

Gly Ala Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly  
20 25 30

Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly  
35 40 45

Ser Asp Val Ser Leu Thr Ala  
50 55

<210> 5  
<211> 129  
<212> DNA  
<213> Homo sapiens

<400> 5  
cagagcaaga tgctgagtgg agtcgggggc ttgtgtctgg gcctgctctt ccttggggcc 60  
  
gggctgttca tctacttcag gaatcagaaa ggacactctg gacttcagcc aagaggattc 120  
  
ctgagctga 129

<210> 6  
<211> 42  
<212> PRT  
<213> Homo sapiens

<400> 6

Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe Val Leu Gly Leu Leu  
1 5 10 15

Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg Asn Gln Lys Gly His  
20 25 30

Ser Gly Leu Gln Pro Arg Gly Phe Leu Ser  
35 40

<210> 7  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Enzyme restriction site

<400> 7  
ctgcaggtcg actctagagg atcc 24

<210> 8  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Enzyme restriction site

<400> 8

Leu Gln Val Asp Ser Arg Gly Ser

1 5

<210> 9

<211> 1683

<212> DNA

<213> Cytomegalovirus

<400> 9

atggagtcgc gcggtcgccg ttgtcccgaa atgatatccg tactgggtcc catttcgggg	60
cacgtgctga aagccgtgtt tagtcgcggc gatacgccgg tgctgccgca cgagacgcga	120
ctctgcaga cgggtatcca cgtacgcgtg agccagccct cgctgatctt ggtatcgcag	180
tacacgcccc actcgacgcc atgccaccgc ggcgacaatc agctgcaggt gcagcacacg	240
tactttacgg gcagcgaggt ggagaacgtg tcggtcaacg tgcacaacct cacgggccga	300
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ctgaacatcc ccagcatcaa cgtgcaccac taccgcgtcg cggccgagcg caaacaccga	420
cacctgcccc tagctgacgc tgtgattcac gcgtcgggca agcagatgtg gcaggcgcgt	480
ctcacggtct cgggactggc ctggacgcgt cagcagaacc agtggaaaga gcccgacgtc	540
tactacacgt cagcgttcgt gtttcccacc aaggacgtgg cactgcggca cgtggtgtgc	600
gcgcacgagc tggtttgctc catggagaac acgcgcgcaa ccaagatgca ggtgataggt	660
gaccagtacg tcaaggtgta cctggagtcc ttctgcgagg acgtgccctc cggcaagctc	720
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ataatcaaac cgggcaagat ctgcgcacatc atgctggatg tggcttttac ctcacacgag	900
cattttgggc tgctgtgtcc caagagcatc ccgggcctga gcattctcagg taacctgttg	960
atgaacgggc agcagatctt cctggaggta caagccatac gcgagaccgt ggaactgcgt	1020
cagtacgatc ccgtggctgc gctcttcttt ttcgatatcg acttgctgct gcagcgcggg	1080
cctcagtaca gegagcacc cacccttcacc agccagtatc gcattccagg caagcttgag	1140
taccgacaca cctgggaccg gcacgacgag ggtgccgccc agggcgacga cgacgtctgg	1200
accagcggat cggactccga cgaagaactc gtaaccaccg agcgcaagac gccccgcgtc	1260
accggcggcg gcgccatggc gggcgcctcc acttccgcgg gccgcaaacg caaatcagca	1320
tcctcggcga cggcgtgcac gtcggggcgtt atgacacgcg gccgccttaa ggccgagtcc	1380

accgtcgcgc ccgaagagga caccgacgag gattccgaca acgaaatcca caatccggcc 1440

gtgttcacct ggccgccttg gcaggccggc atcctggccc gcaacctggt gcccatggtg 1500

gctacggttc agggtcagaa tctgaagtac caggaattct tctgggacgc caacgacatc 1560

taccgcatct tcgccgaatt ggaaggcgta tggcagcccg ctgcgcaacc caaacgtcgc 1620

cgccaccggc aagacgcctt gcccgggcca tgcatgcctt cgacgcccac aaagcaccga 1680

ggt 1683

<210> 10

<211> 561

<212> PRT

<213> Cytomegalovirus

<400> 10

Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser Val Leu Gly

1 5 10 15

Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp Thr

20 25 30

Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val

35 40 45

Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp

50 55 60

Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr

65 70 75 80

Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn

85 90 95

Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr

100 105 110

Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val

115 120 125

His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val

130 135 140

Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg  
145 150 155 160

Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys  
165 170 175

Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys Asp  
180 185 190

Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met  
195 200 205

Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val  
210 215 220

Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu  
225 230 235 240

Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met  
245 250 255

Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe  
260 265 270

Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser  
275 280 285

His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu  
290 295 300

Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu  
305 310 315 320

Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr  
325 330 335

Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Phe Asp  
340 345 350

Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr  
355 360 365

Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr



370

375

380

Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp  
385 390 395 400

Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys  
405 410 415

Thr Pro Arg Val Thr Gly Gly Gly Ala Met Ala Gly Ala Ser Thr Ser  
420 425 430

Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser  
435 440 445

Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro  
450 455 460

Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala  
465 470 475 480

Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu  
485 490 495

Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu  
500 505 510

Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu  
515 520 525

Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln  
530 535 540

Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg  
545 550 555 560

Gly

&lt;210&gt; 11

&lt;211&gt; 1962

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Nucleic acid encoding a fusion protein

<400> 11

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gagacctggg	ccggctccct	gcaggctcgac	tctagaggat	ccaccatgga	gtcgcgcggt	120
cgccgttgtc	ccgaaatgat	atccgtactg	ggccccat	cggggcacgt	gctgaaagcc	180
gtgttttagt	cgggcgatac	gccgggtgct	ccgcacgaga	cgcgactcct	gcagacgggt	240
atccacgtac	gcgtgagcca	gccctcgctg	atcttggtat	cgcagtacac	gcccgactcg	300
acgccatgcc	accgcggcga	caatcagctg	cagggtgcagc	acacgtactt	tacgggcagc	360
gagggtggaga	acgtgtcggg	caacgtgcac	aacccccagg	gccgaagcat	ctgccccagc	420
caggagccca	tgtcgatcta	tgtgtacgcg	ctgccgctca	agatgctgaa	catccccagc	480
atcaacgtgc	accactacc	gtcggcgggc	gagcgcaaac	accgacacct	gcccgtagct	540
gacgctgtga	ttcacgcgtc	gggcaagcag	atgtggcagg	cgcgctctac	gggtctcggga	600
ctggcctgga	cgcgtcagca	gaaccagtgg	aaagagcccg	acgtctacta	cacgtcagcg	660
ttcgtgtttc	ccaccaagga	cgtggcactg	cggcacgtgg	tgtgcgcgca	cgagctggtt	720
tgctccatgg	agaacacgcg	cgcaaccaag	atgcagggtga	taggtgacca	gtacgtcaag	780
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ccccacgagc	gcaacggctt	tacgggtgtt	tgtcccaaaa	atatgataat	caaaccgggc	960
aagatctcgc	acatcatgct	ggatgtggct	tttacctcac	acgagcattt	tgggctgctg	1020
tgtccaaga	gcacccggg	cctgagcatc	tcaggtaacc	tgttgatgaa	cgggcagcag	1080
atcttctctg	aggtacaagc	catacgcgag	accgtggaac	tgcgtcagta	cgatcccggtg	1140
gctgcgctct	tctttttcga	tatcgacttg	ctgctgcagc	gcgggcctca	gtacagcgag	1200
cacccacact	tcaccagcca	gtatcgcatc	cagggaagc	ttgagtaccg	acacacctgg	1260
gaccggcacg	acgagggtgc	cgcccagggc	gacgacgacg	tctggaccag	cggatcggac	1320
tccgacgaag	aactcgtaac	caccgagcgc	aagacgcccc	gcgtcaccgg	cggcggcgcc	1380
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tgcacgtcgg	gcgttatgac	acgcggccgc	cttaaggccg	agtcacacgt	cgcgcccgaa	1500
gaggacaccg	acgaggattc	cgacaacgaa	atccacaatc	cggccgtgtt	cacctggccg	1560
ccctggcagg	ccggcatcct	ggcccgaac	ctggtgccca	tgggtggctac	ggttcagggt	1620

cagaatctga agtaccagga attcttctgg gacgccaacg acatctaccg catcttcgcc 1680  
gaattggaag gcgtatggca gcccgcgtcg caacccaaac gtcgccgcca ccggcaagac 1740  
gccttgcccc ggccatgcat cgctcgacg cccaaaaagc accgaggtgg atccatcgtg 1800  
ggcattgttg ctggcctggc tgtcctagca gttgtgggtca tcggagctgt ggtcgctact 1860  
gtgatgtgta ggaggaagag ctcaggtgga aaaggaggga gctactctca ggctgcgtcc 1920  
agcgacagtg ccagggctc tgatgtgtct ctcacagctt ga 1962

<210> 12  
<211> 653  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion protein

<400> 12

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala  
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser Leu Gln Val Asp Ser Arg  
20 25 30

Gly Ser Thr Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser  
35 40 45

Val Leu Gly Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg  
50 55 60

Gly Asp Thr Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly  
65 70 75 80

Ile His Val Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr  
85 90 95

Thr Pro Asp Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val  
100 105 110

Gln His Thr Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn  
115 120 125

Val His Asn Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met  
130 135 140

Ser Ile Tyr Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser  
145 150 155 160

Ile Asn Val His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His  
165 170 175

Leu Pro Val Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp  
180 185 190

Gln Ala Arg Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn  
195 200 205

Gln Trp Lys Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro  
210 215 220

Thr Lys Asp Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val  
225 230 235 240

Cys Ser Met Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp  
245 250 255

Gln Tyr Val Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser  
260 265 270

Gly Lys Leu Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp  
275 280 285

Leu Thr Met Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg  
290 295 300

Asn Gly Phe Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly  
305 310 315 320

Lys Ile Ser His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His  
325 330 335

Phe Gly Leu Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly  
340 345 350

Asn Leu Leu Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile  
355 360 365

Arg	Glu	Thr	Val	Glu	Leu	Arg	Gln	Tyr	Asp	Pro	Val	Ala	Ala	Leu	Phe	370	375	380	
Phe	Phe	Asp	Ile	Asp	Leu	Leu	Leu	Gln	Arg	Gly	Pro	Gln	Tyr	Ser	Glu	385	390	395	400
His	Pro	Thr	Phe	Thr	Ser	Gln	Tyr	Arg	Ile	Gln	Gly	Lys	Leu	Glu	Tyr	405	410	415	
Arg	His	Thr	Trp	Asp	Arg	His	Asp	Glu	Gly	Ala	Ala	Gln	Gly	Asp	Asp	420	425	430	
Asp	Val	Trp	Thr	Ser	Gly	Ser	Asp	Ser	Asp	Glu	Glu	Leu	Val	Thr	Thr	435	440	445	
Glu	Arg	Lys	Thr	Pro	Arg	Val	Thr	Gly	Gly	Gly	Ala	Met	Ala	Gly	Ala	450	455	460	
Ser	Thr	Ser	Ala	Gly	Arg	Lys	Arg	Lys	Ser	Ala	Ser	Ser	Ala	Thr	Ala	465	470	475	480
Cys	Thr	Ser	Gly	Val	Met	Thr	Arg	Gly	Arg	Leu	Lys	Ala	Glu	Ser	Thr	485	490	495	
Val	Ala	Pro	Glu	Glu	Asp	Thr	Asp	Glu	Asp	Ser	Asp	Asn	Glu	Ile	His	500	505	510	
Asn	Pro	Ala	Val	Phe	Thr	Trp	Pro	Pro	Trp	Gln	Ala	Gly	Ile	Leu	Ala	515	520	525	
Arg	Asn	Leu	Val	Pro	Met	Val	Ala	Thr	Val	Gln	Gly	Gln	Asn	Leu	Lys	530	535	540	
Tyr	Gln	Glu	Phe	Phe	Trp	Asp	Ala	Asn	Asp	Ile	Tyr	Arg	Ile	Phe	Ala	545	550	555	560
Glu	Leu	Glu	Gly	Val	Trp	Gln	Pro	Ala	Ala	Gln	Pro	Lys	Arg	Arg	Arg	565	570	575	
His	Arg	Gln	Asp	Ala	Leu	Pro	Gly	Pro	Cys	Ile	Ala	Ser	Thr	Pro	Lys	580	585	590	

Lys His Arg Gly Gly Ser Ile Val Gly Ile Val